

This paper investigates the dynamics of epidemic spread on two prototypical static network structures: Erdős–Rényi random graph and Barabási–Albert scale-free network.

**Introduction** The study of infectious disease spread over complex networks has revealed profound effects of network topology on the dynamics of epidemics.

**Methodology** Modeling Framework We model epidemic dynamics using the SIR (Susceptible-Infected-Recovered) paradigm.

Erdős–Rényi (ER) random graph:  $N = 1000$  nodes, mean degree  $\langle k \rangle = 8$ . Each pair of nodes is connected independently with probability  $p = \frac{1}{N}$ .

Barabási–Albert (BA) scale-free network:  $N = 1000$  nodes, each new node attaches to  $m = 4$  existing nodes; asymptotically, the distribution of node degrees follows a power law.

Both networks are generated using the NetworkX package, with degree distributions shown in Figure 1.

Disease dynamics proceed according to:

Infection: Susceptible nodes connect to their Infected neighbors and become infected at rate  $\beta$  per Infectious-Susceptible edge.

Recovery: Infected nodes recover at rate  $\gamma$  per unit time, entering the Removed class (immune).

Parameters are set to match  $R_0 = 2.5$  using Newman's result for network epidemics:

where  $\langle k^2 \rangle$  is the second degree moment. For both networks,  $\gamma = 0.2$ ,  $R_0 = 2.5$ , and  $N = 1000$ .  $\beta$  is computed individually for each network.

Initial conditions are set as 1% infected (10 nodes), 99% susceptible, 0% recovered, distributed randomly.

Simulation and analysis are implemented in Python using FastGEMF for SIR process, with results output for five stochastic simulations.

[h!] [width=0.45]degdist\_ER.png[width = 0.45]degdist\_BA.pngDegree distributions for Erdős–Rényi(left) and Barabási–Albert(right)

[h!] Network degree statistics and SIR parameters  
ER:  $\langle k \rangle = 8.04$ ,  $\langle k^2 \rangle = 72.48$ ,  $\beta = 0.062$   
BA:  $\langle k \rangle = 7.97138$ ,  $\langle k^2 \rangle = 0.020.031$

Results Simulation outputs for both networks are summarized in Figure 2 (time evolution of  $S$ ,  $I$ ,  $R$ ) and Table 1 (quantitative metrics).

**Final epidemic size:** In ER network, 773 individuals out of 1000 were eventually infected (entered  $R$  class), compared to 341 in BA.

**Peak infection:** Peak prevalence was much higher in ER (185) than in BA (64), and occurred sooner (18.3 days vs 21.3 days).

**Epidemic duration:** Epidemic lasted  $\sim 64$  days in ER and  $\sim 59$  days in BA.

**Doubling time** (early phase): Disease spread twice as fast in ER (1.47 days) than in BA (3.48 days).

[h!] [width=0.48]results-11.png [width=0.48]results-12.png Compartment trajectories  $S$ ,  $I$ ,  $R$  vs time for (left) ER network and (right) BA network.

Metric	ER	BA
Final epidemic size ( $R_{final}$ )	773	341
Peak infection	185	64
Time of peak	18.3 days	21.3 days
Epidemic duration	64.1 days	59.2 days
Doubling time	1.47 days	3.48 days

Discussion The results confirm and quantify strong effects of network topology on the progression and societal burden of epidemics.

The epidemic threshold is determined by the network's degree distribution, particularly the mean excess degree  $q = (\langle k^2 \rangle - \langle k \rangle)$ .

The implications are practical: for networks with heavy-tailed degree distributions, conventional  $R_0$ -based interventions may be less effective.

Conclusion This comparative study demonstrates that even under identical epidemiological parameters, the underlying network structure can have a significant impact on epidemic dynamics.

\*References 99

M. E. J. Newman, "The spread of epidemic disease on networks," Phys. Rev. E, vol. 66, no. 1, p. 016128, 2002. Available: <https://doi.org/10.1103/PhysRevE.66.016128>

M.J. Keeling, "Implications of network structure for epidemic dynamics," Theor. Popul. Biol., vol. 67, pp. 1–8, 2005. doi:10.1016/j.tpb.2004.09.001

Supplementary Figures Degree Distributions [h!] [width=0.45]degdist\_ER.png[width = 0.45]degdist\_BA.pngDegree distributions for Erdős–Rényi(left) and Barabási–Albert(right)

Code Excerpts Network and simulation codes are included as supplementary files:

network\_construction.py, parameter\_setting.py, simulation-11.py, simulation-12.py, analysis\_ER.py, analysis\_BA.py.